SRNT

Sequence Match Listing for SEQ ID NO 42

Mon Mar 24 09:16:41 2003

us-09-97

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RESULT 1
NKG7_HUMAN
ID   NKG7_HUMAN     STANDARD;      PRT;   165 AA.
AC   Q16617;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein NKG7 (Natural killer cell protein 7) (G-CSF-induced gene 1
DE   protein) (Protein GIG-1).
GN   NKG7 OR GIG1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93209815; PubMed=8458737;
RA   Turman M.A., Yabe T., McSherry C., Bach F.H., Houchins J.P.;
RT   "Characterization of a novel gene (NKG7) on human chromosome 19 that
RT   is expressed in natural killer cells and T cells.";
RL   Hum. Immunol. 36:34-40(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94168584; PubMed=7510105;
RA   Shimane M., Tani K., Maruyama K., Takahashi S., Ozawa K., Asano S.;
RT   "Molecular cloning and characterization of G-CSF induced gene cDNA.";
RL   Biochem. Biophys. Res. Commun. 199:26-32(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Church R.L., Li X.L., Wang J.H.;
RT   "Human chromosome 19q13.4 DNA sequence, including complete sequence
RT   for LIM2 and NKG7.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED T CELLS, IN KIDNEY,
CC       LIVER, LUNG AND PANCREAS. NOT EXPRESSED IN BRAIN, HEART, OR
CC       SKELETAL MUSCLE. EXPRESSED AT HIGH LEVELS IN TCR GAMMA DELTA-
CC       EXPRESSING CTL CLONES, AND IN SOME TCR ALPHA BETA-EXPRESSING CTL
CC       CLONES (BOTH CD4+ AND CD8+), BUT IS NOT EXPRESSED IN OTHER TCR
CC       ALPHA BETA-EXPRESSING CTL CLONES AND IN CELL LINES REPRESENTING B
CC       CELLS, MONOCYTES, AND MYELOID CELLS.
CC   -!- INDUCTION: BY G-CSF.
CC   -!- SIMILARITY: BELONGS TO THE PMP-22 / EMP / MP20 FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; U09608; AAA18209.1; -.
DR   EMBL; S69115; AAB30078.1; -.
DR   EMBL; AF305941; AAG32329.1; -.
DR   EMBL; BC015759; AAH15759.1; -.
DR   Genew; HGNC:7830; NKG7.
DR   MIM; 606008; -.
DR   InterPro; IPR004031; PMP22_Claudin.
DR   InterPro; IPR004032; PMP22_EMP_MP20.
DR   Pfam; PF00822; PMP22_Claudin; 1.
DR   PROSITE; PS01221; PMP22_1; FALSE_NEG.
DR   PROSITE; PS01222; PMP22_2; FALSE_NEG.
KW   Transmembrane.
FT   TRANSMEM      9     29       POTENTIAL.
FT   TRANSMEM     61     81       POTENTIAL.
FT   TRANSMEM     92    112       POTENTIAL.
FT   TRANSMEM    133    153       POTENTIAL.
SQ   SEQUENCE   165 AA;  17664 MW;  CEE2901B6DC42A6C CRC64;

  Query Match             40.9%;  Score 325.5;  DB 1;  Length 165;
  Best Local Similarity   65.3%;  Pred. No. 3.1e-21;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels   35;  Gaps    1;

Qy       1 MELCRSLALLGGSLGLMFCLIALSTDFWFEAVGPTHSAHSGLWPTGHGDIIS-------- 52
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MELCRSLALLGGSLGLMFCLIALSTDFWFEAVGPTHSAHSGLWPTGHGDIISGYIHVTQT 60

Qy      53 --------------------------GHGPLVSTTAAFAA 66
                                     ||||||||||||||
Db      61 FSIMAVLWALVSVSFLVLSCFPSLPPPGHGPLVSTTAAFAA 101
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